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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Thu 6 Apr 106 10:05:38 -PST

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

- 4. US-10-756-778-8 (1-492)
- 1. US-10-756-778-2 (1-742)

Region Alignment: (listed in Clustered order)

US-10-756- 1 mdfsmysseqkypdnnngelicesefyadctnemkkyhpiegdlkfangefdnyyq
consensus mdfsmysseqkypdnnngelicesefyadctnemkkyhpiegdlkfangefdnyyq
US-10-756- 1
US-10-756- 62 hsdvsnaygmktelivntdiptynlninamntlcridlpetmsiydnlrstvcvpsfen
consensus hsdvsnaygmktelivntdiptynlninamntlcridlpetmsiydnlrstvcvpsfen
US-10-756- 7 TG viTQ
US-10-756- 123 qfdpikfihdieleiaetgsfalsTQsmnggtrdiapmlistcfxvagsllpfpislgal
consensus qfdpikfihdieleiaetgsfalsTQsmnggtrdiapmlistcfxvagsllpfpislgal
US-10-756- 13 FRI IndNFI
US-10-756- 184 asfeyvdsqgtgamanlwrqwdvveRidekil--NFlmgaelaanaalkeyarvki
consensus asfeyvdsqgtgamanlwrqwdvveRidekil--NFlmgaelaanaalkeyarvki
US-10-756- 22 KYIAKIQSTNOSDLOYPVLTPLRAQACVMHLM
US-10-756- 245 endmrtiaepstgvtlqftrIndnfiKYIAKIQSTNOSDLOYPVLTPLRAQACVMHLM
consensus endmrtiaepstgvtlqftrIndnfiKYIAKIQSTNOSDLOYPVLTPLRAQACVMHLM
US-10-756- 56 LKDATTSVWGQOIDSQQLNGYKAEILRLIKVYTNVNTYNNQGLELEKAKPLANSDBPEY
US-10-756- 306 LKDATTSVWGQOIDSQQLNGYKAEILRLIKVYTNVNTYNNQGLELEKAKPLANSDBPEY
consensus LKDATTSVWGQOIDSQQLNGYKAEILRLIKVYTNVNTYNNQGLELEKAKPLANSDBPEY

US-10-756- 117 LQAGRPDISVLRNSKEVWKKNNKVAKYRGMAKMSLSLAALPFRGPNVPRQALKVQSRQ
US-10-756- 367 LQAGRPDISVLRNSKEVWKKNNKVAKYRGMAKMSLSLAALPFRGPNVPRQALKVQSRQ
consensus LQAGRPDISVLRNSKEVWKKNNKVAKYRGMAKMSLSLAALPFRGPNVPRQALKVQSRQ
US-10-756- 178 IFAPVIGIPGIGITSDSGPTFGSMRFVDVKTVDQIDALRQMLVLYIQPLKSAVFWIYESDMK
US-10-756- 428 IFAPVIGIPGIGITSDSGPTFGSMRFVDVKTVDQIDALRQMLVLYIQPLKSAVFWIYESDMK
consensus IFAPVIGIPGIGITSDSGPTFGSMRFVDVKTVDQIDALRQMLVLYIQPLKSAVFWIYESDMK
US-10-756- 239 VRATVYNDYIGKRGSGNTGAAMHMSSDPSALYTSALGAAGYAPNVVGVRYSHGGSYTKGMA
US-10-756- 489 VRATVYNDYIGKRGSGNTGAAMHMSSDPSALYTSALGAAGYAPNVVGVRYSHGGSYTKGMA
consensus VRATVYNDYIGKRGSGNTGAAMHMSSDPSALYTSALGAAGYAPNVVGVRYSHGGSYTKGMA
US-10-756- 300 PANTNAYAPFEFKYPGYTLHSVSAVGLSKAPDADSVMFGRPVLLNEANQLLTDALQI
US-10-756- 550 PANTNAYAPFEFKYPGYTLHSVSAVGLSKAPDADSVMFGRPVLLNEANQLLTDALQI
consensus PANTNAYAPFEFKYPGYTLHSVSAVGLSKAPDADSVMFGRPVLLNEANQLLTDALQI
US-10-756- 361 PAEIGITDVVPAFGRTPEPINGODAIRIWESFTSGFPTTVVDSPOKOKYRIYRIANNLS
US-10-756- 611 PAEIGITDVVPAFGRTPEPINGODAIRIWESFTSGFPTTVVDSPOKOKYRIYRIANNLS
consensus PAEIGITDVVPAFGRTPEPINGODAIRIWESFTSGFPTTVVDSPOKOKYRIYRIANNLS
US-10-756- 422 ASTVSLTYNNQTFPTDILNTSLDPNGVRGNGSYTLVHGPIIEFSQGTNIFKLQSQKEFA
US-10-756- 672 ASTVSLTYNNQTFPTDILNTSLDPNGVRGNGSYTLVHGPIIEFSQGTNIFKLQSQKEFA
consensus ASTVSLTYNNQTFPTDILNTSLDPNGVRGNGSYTLVHGPIIEFSQGTNIFKLQSQKEFA
US-10-756- 483 IDSIIIFSPV
US-10-756- 733 IDSIIIFSPV
consensus IDSIIIFSPV
Alignment score = -768.00
Scoring matrix:

4	1
1	-768

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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Thu 6 Apr 106 10:06:28-PR

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

4. US-10-756-778-8 (1-492)
7. US-10-756-778-13 (1-492)

Region Alignment: (listed in Clustered order)

US-10-756- 1 IAEPPSTGVITQRIINDNFIKYIAKQFSTNOSDLOQYVLTLPRAQACVHMLMLKDAT
US-10-756- 1 XAEPPSTGVITQRIINDNFIKYIAKQFSTNOSDLOQYVLTLPRAQACVHMLMLKDAT
consensus -AEPPSTGVITQRIINDNFIKYIAKQFSTNOSDLOQYVLTLPRAQACVHMLMLKDAT

US-10-756- 62 TSVWGQIQIDISQQLNGYKAEILIRLIKVTNDVNTTNOGLEEKAKPLNYSDBEYIQAQRP
US-10-756- 62 TSVWGQIQIDISQQLNGYKAEILIRLIKVTNDVNTTNOGLEEKAKPLNYSDBEYIQAQRP
consensus TSVWGQIQIDISQQLNGYKAEILIRLIKVTNDVNTTNOGLEEKAKPLNYSDBEYIQAQRP

US-10-756- 123 DISVLRSNPFKEVWKAKVAKYKRGMAWSALSLAALPPTFGPNYPKQALKVQSRQIFAPVI
US-10-756- 123 DISVLRSNPFKEVWKAKVAKYKRGMAWSALSLAALPPTFGPNYPKQALKVQSRQIFAPVI
consensus DISVLRSNPFKEVWKAKVAKYKRGMAWSALSLAALPPTFGPNYPKQALKVQSRQIFAPVI

US-10-756- 184 GIPGGITISODSPTFGSMRFVYKTYDQIDALRGLMELYIQPLKSAFPIYESDMKVRATYV
US-10-756- 184 GIPGGITISODSPTFGSMRFVYKTYDQIDALRGLMELYIQPLKSAFPIYESDMKVRATYV
consensus GIPGGITISODSPTFGSMRFVYKTYDQIDALRGLMELYIQPLKSAFPIYESDMKVRATYV

US-10-756- 245 NDYIGRGSNTGAMAMWSSDPSAIYTSALGAAGYAPNVVGVRYSHGGSYTKGMAPANTNA
US-10-756- 245 NDYIGRGSNTGAMAMWSSDPSAIYTSALGAAGYAPNVVGVRYSHGGSYTKGMAPANTNA
consensus NDYIGRGSNTGAMAMWSSDPSAIYTSALGAAGYAPNVVGVRYSHGGSYTKGMAPANTNA

US-10-756- 306 YAPFEKYPGYKLIHSYSAVGLSKAPDADSVMFGFRPVLLLENANQLTDTALQIPAEIGI
US-10-756- 306 YAPFEKYPGYKLIHSYSAVGLSKAPDADSVMFGFRPVLLLENANQLTDTALQIPAEIGI
consensus YAPFEKYPGYKLIHSYSAVGLSKAPDADSVMFGFRPVLLLENANQLTDTALQIPAEIGI

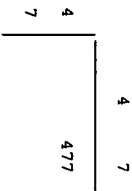
US-10-756- 367 TDVVPAFGRTPEEPINGODAIrIWESFTSGFGFTYVDSPQOKXKIIYRIANNLSASTVSL
US-10-756- 367 TDVVPAFGRTPEEPINGODAIrIWESFTSGFGFTYVDSPQOKXKIIYRIANNLSASTVSL
consensus TDVVPAFGRTPEEPINGODAIrIWESFTSGFGFTYVDSPQOKXKIIYRIANNLSASTVSL

US-10-756- 428 TYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPIIEFSOGTNIFFKLGSQKGEFAIDSIIIF
US-10-756- 428 TYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPIIEFSOGTNIFFKLGSQKGEFAIDSIIIF
consensus TYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPIIEFSOGTNIFFKLGSQKGEFAIDSIIIF

US-10-756- 489 SPV
US-10-756- 489 SPV
consensus SPV

Alignment score = 477.00

Scoring matrix:



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Release 5.4

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Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off

AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

4. US-10-756-778-8 (1-492)
8. US-10-756-778-14 (1-742)

Region Alignment: (listed in clustered order)

```
US-10-756- 1 mdpfmsyseqkypdnnngelltxsasydctnenukxynhpiegdlkfxnqefkdxnyq
consensus
US-10-756- 1 mdpfmsyseqkypdnnngelltxsasydctnenukxynhpiegdlkfxnqefkdxnyq
consensus
US-10-756- 62 hedvnsygmktelvnctdlypnctnxinsmrcnlcxdlppecmsiydnlrctvtvpfsfn
consensus
US-10-756- 1 hedvnsygmktelvnctdlypnctnxinsmrcnlcxdlppecmsiydnlrctvtvpfsfn
consensus
US-10-756- 123 qfdqplkflndieiaixtgsfaalcgennmggtcdixpmlisctffkvaxslpfpjsslgai
consensus
US-10-756- 1 qfdqplkflndieiaixtgsfaalcgennmggtcdixpmlisctffkvaxslpfpjsslgai
consensus
US-10-756- 184 asfyyvdsqgtgamanlwrgmvdvvekrldsklidyhnfimgaelaainaslkeyarvvkif
consensus
US-10-756- 1 asfyyvdsqgtgamanlwrgmvdvvekrldsklidyhnfimgaelaainaslkeyarvvkif
consensus
US-10-756- 1 IAPPSTGVITGFRILNDNFIKYIAKLQFSTNSDLYPVLTLPLRAQACVWHLM
US-10-756- 245 endmnrxaEPSTGVITGFRILNDNFIKYIAKLQFSTNSDLYPVLTLPLRAQACVWHLM
consensus
US-10-756- 56 LKDATTSVWGQIDISQQLNGYKAEILIRLIKVTYNDVNTTNGLELEKAKPLANSDEPEY
US-10-756- 306 LKDATTSVWGQIDISQQLNGYKAEILIRLIKVTYNDVNTTNGLELEKAKPLANSDEPEY
consensus
LKDATTSVWGQIDISQQLNGYKAEILIRLIKVTYNDVNTTNGLELEKAKPLANSDEPEY
```

```
US-10-756- 117 LQAGRPDISVLRNFKEMKMKVAKYIKRGAMASLSLALPFTFGNNYKQALKVVOSSHQ
US-10-756- 367 LQAGRPDISVLRNFKEMKMKVAKYIKRGAMASLSLALPFTFGNNYKQALKVVOSSHQ
consensus
LQAGRPDISVLRNFKEMKMKVAKYIKRGAMASLSLALPFTFGNNYKQALKVVOSSHQ

US-10-756- 178 IFAPVIGIPGIGTSQDESPITFGSNRPDVKTYYDIDALRGLMELYIOPLKSAYF*IYESDMK
US-10-756- 428 IFAPVIGIPGIGTSQDESPITFGSNRPDVKTYYDIDALRGLMELYIOPLKSAYF*IYESDMK
consensus
IFAPVIGIPGIGTSQDESPITFGSNRPDVKTYYDIDALRGLMELYIOPLKSAYF*IYESDMK

US-10-756- 239 VRATYVNDYIGKRGSGNTGAMHWSDDPSAIYTSALGAAGYAPNVVGVRRYSHGGSYTKGMA
US-10-756- 489 VRATYVNDYIGKRGSGNTGAMHWSDDPSAIYTSALGAAGYAPNVVGVRRYSHGGSYTKGMA
consensus
VRATYVNDYIGKRGSGNTGAMHWSDDPSAIYTSALGAAGYAPNVVGVRRYSHGGSYTKGMA

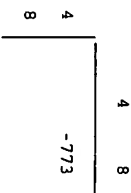
US-10-756- 300 PANTNAYAPPEFKYPGYKLSVSAYGLSKAPDADSVMGFRPVLLLENANQLITDIALOI
US-10-756- 550 PANTNAYAPPEFKYPGYKLSVSAYGLSKAPDADSVMGFRPVLLLENANQLITDIALOI
consensus
PANTNAYAPPEFKYPGYKLSVSAYGLSKAPDADSVMGFRPVLLLENANQLITDIALOI

US-10-756- 361 PAEIGITDVVPAFGRTPEPINGODAI*IWESFTSGFGFTYTVDSPOKOKYKIIYRIANLNS
US-10-756- 611 PAEIGITDVVPAFGRTPEPINGODAI*IWESFTSGFGFTYTVDSPOKOKYKIIYRIANLNS
consensus
PAEIGITDVVPAFGRTPEPINGODAI*IWESFTSGFGFTYTVDSPOKOKYKIIYRIANLNS

US-10-756- 422 ASTVSLTYNNOTFTDILNTSLDPNGVRGNVGSYTLVEGPIIEFSQGTNIIFKLGSQGEFA
US-10-756- 672 ASTVSLTYNNOTFTDILNTSLDPNGVRGNVGSYTLVEGPIIEFSQGTNIIFKLGSQGEFA
consensus
ASTVSLTYNNOTFTDILNTSLDPNGVRGNVGSYTLVEGPIIEFSQGTNIIFKLGSQGEFA

US-10-756- 483 IDSIIIFSPVY
US-10-756- 733 IDSIIIFSPVX
consensus
IDSIIIFSPV-

Alignment score = -773.00
Scoring matrix:
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IntelliGenetics

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Thu 6 Apr 106 10:06:52-PST

Solution Parameters:

Amino Alphabet	= Identity
Output line length	= 80
Compress	= Off
Histogram	= Off
Randomization	= Off
AMINO-Res-length	= 2
Deletion-weight	= 5.00
Length-factor	= 0
Matching-weight	= 1.00
NUCLEIC-Res-length	= 4
Spread-factor	= 50

Clustered order of selected sequences:

4. US-10-756-778-8 (1-492)
9. US-10-756-778-15 (1-492)

Region Alignment: (listed in clustered order)

US-10-756- 1 IAEPSGTGVTGFRILNDFIKIAKQGSTNQSDQIPVTLPLRAQACMHHMLLKQAT
| | | | |
US-10-756- 1 XAEPSGTGVTGFRILNDFIKIAKQGSTNQSDQIPVTLPLRAQACMHHMLLKQAT
| | | | |
consensus -AEPSGTGVTGFRILNDFIKIAKQGSTNQSDQIPVTLPLRAQACMHHMLLKQAT

US-10-756- 52 TSWMGQIDISQGLNGKAEFLRLIKVYNDVVTTYNQGLELEKAKPLNYSDPSEYTQAAGRPR
|||
US-10-756- 62 TSWMGQIDISQGLNGKAEFLRLIKVYNDVVTTYNQGLELEKAKPLNYSDPSEYTQAAGRPR
|||
consensus TSWMGQIDISQGLNGKAEFLRLIKVYNDVVTTYNQGLELEKAKPLNYSDPSEYTQAAGRPR

US-10-756- 123 DISVLRSNPKEMKKN-VAKYKRGMAALSIALALPFPGNGNYPRKALKTVQSOIFAIVIT
|||
US-10-756- 123 DISVLRSNPKEMKKN-VAKYKRGMAALSIALALPFPGNGNYPRKALKTVQSOIFAIVIT
DISVLRSNPKEMKKN-VAKYKRGMAALSIALALPFPGNGNYPRKALKTVQSOIFAIVIT

US-10-756- 184 G1RGGITSDDSPPTGSKRFVYKTDQIDALRQIMELTYIQLPKAYF-IYESDMKVATTV
|||
US-10-756- 184 G1RGGITSDDXXCTGSKRFVYKTDQIDALRQIMELTYIQLPKAYF-IYESDMKVATTV
|||
consensus G1RGGITSDD--TFSGRFVYKTDQIDALR-IMELTYIQLPKAYF-IYESDMKVATTV

US-10-756- 245 NDYIGKRGSGNTCAAHMMSDPS.IYTSALGAGTAPNVVGVR.YSHGGSYTKGMAP.PANTNA
US-10-756- 245 NDYIGKRGSGNTCAAHMMSDPS.IYTSALGAGTAPNVVGVR.YSHGGSYTKGMAP.PANTNA
Consensus NDYIGKRGSGNTC-AH-MMSDPS-IYTSALGAGTAPNVVGVR.YSHGGSYTKGMAP-NTNA

US-10-756- 306 YAPFPERKPYGLTHSVSAGLSKAPDADSVNFGRRPVLTLENEANQLITDTAQIPAEIGI
US-10-756- 306 YAPFPERKPYGLTHSVSAGLSKAPDADSVNFGRRPVLTLENEANQLITDTAQIPAEIGI
consensus YAPFPERKPYGLTHSVSAGLSKAPDADSVNFGRRPVLTLENEANQLITDTAQIPAEIGI

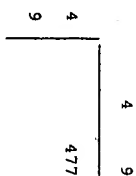
Accession	Sequence
US-10-756-367	TDVVPAFGRTPEEPINGDQALIMESFISGSGFFYYTDSPOKQKXKIIYRIANNLSASTVSL
US-10-756-367	TDVVPAFGRTPEEPINGDQALIMESFISGSGFFYYTDSPOKQKXKIIYRIANNLSASTVSL
Consensus	TDVVPAFGRTPEEPINGDQALIMESFISGSGFFYYTDSPOKQKXKIIYRIANNLSASTVSL

	US-10-756-	428	TNNQTFPTDLNTSLDPNGRVGYSGYTLVEGIIIEFSOGTNI PKLxSOKGEPAIDISITIF
	US-10-756-	428	TNNQTFPTDLNTSLDPNGRVGYSGYTLVEGIIIEFSOGTNI PKLxSOKGEPAIDISITIF
	consensus		TNNQTFPTDLNTSLDPNGRVGYSGYTLVEGIIIEFSOGTNI PKL-SOKGEPAIDISITIF

US-10-756-	489	SPVV
US-10-756-	489	SPVX
consensus		SPV-

Alignment score = 477.00

Scoring matrix:



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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

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Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

4. US-10-756-778-8 (1-492)
10. US-10-756-778-18 (232-723)

Region Alignment: (listed in Clustered order)

US-10-756- 1 |AEPSTGVITQRIINDNFIKYIAKLQSTNOSDLOQVPLTLPPLAQACVWHMLMLKDAT
US-10-756- 1 |AEPSTGVITQRIINDNFIKYIAKLQSTNOSDLOQVPLTLPPLAQACVWHMLMLKDAT
US-10-756- 1 |AEPSTGVITQRIINDNFIKYIAKLQSTNOSDLOQVPLTLPPLAQACVWHMLMLKDAT
consensus -AEPSTGVITQRIINDNFIKYIAKLQSTNOSDLOQVPLTLPPLAQACVWHMLMLKDAT
US-10-756- 62 |TSVWGQOIDSQOLNGYKAEILIRLIKYYTNDVNTTNOGLEEKAPLNTSDPEEYIQAGR
US-10-756- 62 |TSVWGQOIDSQOLNGYKAEILIRLIKYYTNDVNTTNOGLEEKAPLNTSDPEEYIQAGR
consensus TSVWGQOIDSQOLNGYKAEILIRLIKYYTNDVNTTNOGLEEKAPLNTSDPEEYIQAGR
US-10-756- 123 |DISVLRSNFKKWKNNVAKYKRGAMMSALSIALFPFTGPNYPKQALKVQSRQIFAPVI
US-10-756- 123 |DISVLRSNFKKWKNNVAKYKRGAMMSALSIALFPFTGPNYPKQALKVQSRQIFAPVI
consensus DISVLRSNFKKWKNNVAKYKRGAMMSALSIALFPFTGPNYPKQALKVQSRQIFAPVI
US-10-756- 184 |GIPGGITSDQDSGPTFGSMRFDVKTVDQIDALRLMELYIOPLSAYF*IYESDMKVRATYV
US-10-756- 184 |GIPGGITSDQDSGPTFGSMRFDVKTVDQIDALRLMELYIOPLSAYF*IYESDMKVRATYV
consensus GIPGGITSDQDSGPTFGSMRFDVKTVDQIDALRLMELYIOPLSAYF*IYESDMKVRATYV
US-10-756- 245 |NDYIGKRGSGNTGAAMHMSDPSAITYSALGAAGYAPNVVGVRYSHGGSYTKGMAPANTNA
US-10-756- 245 |NDYIGKRGSGNTGAAMHMSDPSAITYSALGAAGYAPNVVGVRYSHGGSYTKGMAPANTNA
consensus NDYIGKRGSGNTG-AM-HMSDPS-ITYSALGAAGYAPNVVGVRYSHGGSYTKGMAP-NTNA
US-10-756- 306 |YAPFEKYPGYKLHVSAYGLSKAPD-ADSVMEGFRPVLLBNBANQLTDTALQIPAEIGI
US-10-756- 306 |YAPFEKYPGYKLHVSAYGLSKAPD-ADSVMEGFRPVLLBNBANQLTDTALQIPAEIGI
consensus YAPFEKYPGYKLHVSAYGLSKAPD-ADSVMEGFRPVLLBNBANQLTDTALQIPAEIGI

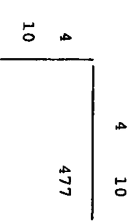
US-10-756- 367 |TDVVPARGRTPEEPINGODAI-IWESFTSGFGFTYVDSPOKOKKIIYRIANNLSASTVSL
US-10-756- 367 |TDVVPARGRTPEEPINGODAI-IWESFTSGFGFTYVDSPOKOKKIIYRIANNLSASTVSL
consensus TDVVPARGRTPEEPINGODAI-IWESFTSGFGFTYVDSPOKOKKIIYRIANNLSASTVSL

US-10-756- 428 |TYNNQTFPTDILNTSLDPNGVRNGYSYTLVEGPIIEFSQGTNIFKLGSQKGEPAIDSIIF
US-10-756- 428 |TYNNQTFPTDILNTSLDPNGVRNGYSYTLVEGPIIEFSQGTNIFKLGSQKGEPAIDSIIF
consensus TYNNQTFPTDILNTSLDPNGVRNGYSYTLVEGPIIEFSQGTNIFKLGSQKGEPAIDSIIF

US-10-756- 489 SPV
US-10-756- 489 SPV
consensus SPV

Alignment score = 477.00

Scoring matrix:



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320      330      340      350      360      370      380
FKYPKYKHSYSAVGLSTAPPAADSVWGFRPULLLENANQLDTALQIPAEIGTDVPAFRTEEPING
|||||
FKRIPYKHSYSAVGLSTAPPAADSVWGFRPULLLENANQLDTALQIPAEIGTDVPAFRTEEPING
570      580      590      600      610      620      630
ODAIRWESFTSGFRFTYVDSPOKOKKITYRIANMLASTVSLTNNQFFTDILNTSLDPNGVRNGYS
|||||
ODAIRWESFTSGFRFTYVDSPOKOKKITYRIANMLASTVSLTNNQFFTDILNTSLDPNGVRNGYS
640      650      660      670      680      690      700
460      470      480      490 X
YTLVEGPTEESOGTNIPIKLSOGKGFADISITSPVY
|||||
YTLVEGPTEESOGTNIPIKLSOGKGFADISITSPVY
710      720      730      740 X

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2. US-10-756-778-8 (2-492) US-10-756-778-15 Sequence 15, Application US/10756778

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Sequence 15, Application US/10756778
GENERAL INFORMATION:
APPLICANT: Agriculture Agroalimentaire Canada
APPLICANT: Cote, Jean-Charles
APPLICANT: Mizuki, Elichi
APPLICANT: Akao, Tetsuyuki
TITLE OF INVENTION: A NOVEL BACILLUS THURINGIENSIS STRAIN, CRYSTAL GENE AND CRYSTAL
FILE REFERENCE: 12292.5
CURRENT APPLICATION NUMBER: US/10756,778
PRIOR FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 2,410,153
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.2
SEQ ID NO 15
LENGTH: 492
TYPE: PRF
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: Xaa= isoleucine or methionine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (139)..(139)
OTHER INFORMATION: lysine or arginine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (194)..(194)
OTHER INFORMATION: Xaa= serine or histidine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (195)..(195)
OTHER INFORMATION: Xaa= glycine or serine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (196)..(196)
OTHER INFORMATION: Xaa= glycine or proline
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (216)..(216)
OTHER INFORMATION: Xaa= glutamine or arginine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (231)..(231)
OTHER INFORMATION: Xaa= tyrosine or tryptophan
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (257)..(257)

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OTHER INFORMATION: Xaa= alanine or leucine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (260)..(260)
OTHER INFORMATION: Xaa= glycine or histidine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (268)..(268)
OTHER INFORMATION: Xaa= alanine or valine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (301)..(301)
OTHER INFORMATION: Xaa= alanine or proline
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (387)..(387)
OTHER INFORMATION: Xaa= arginine or isoleucine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (475)..(475)
OTHER INFORMATION: Xaa= glycine or arginine
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (492)..(492)
OTHER INFORMATION: Xaa= valine or serine

Initial Score = 477 Optimized Score = 477 Significance = -0.33
Residue Identity = 96% Matches = 477 Mismatches = 15
Gaps = 0 Conservative Substitutions = 0

```

```

X      10      20      30      40      50      60      70
IAPBPGVITGPRRIINDPFIKXIYAKLQSTNSDLOQYVLTLPRAQACVWMLMLKQATTSVWGQIDISQ
XAPBPGVITGPRRIINDPFIKXIYAKLQSTNSDLOQYVLTLPRAQACVWMLMLKQATTSVWGQIDISQ
X      10      20      30      40      50      60      70

```

```

QNLGYAEILIRLIKVTYNDVNTYNOGLELEKAKPLNYSDBEYIQAQGPDISVLRSNKEXVWKNKVAKYX
QNLGYAEILIRLIKVTYNDVNTYNOGLELEKAKPLNYSDBEYIQAQGPDISVLRSNKEXVWKNKVAKYX
QNLGYAEILIRLIKVTYNDVNTYNOGLELEKAKPLNYSDBEYIQAQGPDISVLRSNKEXVWKNKVAKYX
80      90      100      110      120      130      140

```

```

RGWMSALSLAALPFTFGSNYPKQALKVQSRQIFAPVIGIGITSDSGPTFSMRPDVXTYQIDALRQ
RGWMSALSLAALPFTFGSNYPKQALKVQSRQIFAPVIGIGITSDSGPTFSMRPDVXTYQIDALRQ
RGWMSALSLAALPFTFGSNYPKQALKVQSRQIFAPVIGIGITSDSGPTFSMRPDVXTYQIDALRQ
150      160      170      180      190      200      210

```

```

LMELYIQLKSAIFWYIESDWRATYVDYIGKGSNTGAAMHWSDDPSAIYTSALGAAYAPVVGVRX
LMELYIQLKSAIFWYIESDWRATYVDYIGKGSNTGAAMHWSDDPSAIYTSALGAAYAPVVGVRX
LMELYIQLKSAIFWYIESDWRATYVDYIGKGSNTGAAMHWSDDPSAIYTSALGAAYAPVVGVRX
220      230      240      250      260      270      280

```

```

SHGGSTYKGAAPANTNAVAPFEFKYPGYKLSHVSAYGLSKAPDAADSVWFRPYLLENANQLDTALQI
SHGGSTYKGAAPANTNAVAPFEFKYPGYKLSHVSAYGLSKAPDAADSVWFRPYLLENANQLDTALQI
SHGGSTYKGAAPANTNAVAPFEFKYPGYKLSHVSAYGLSKAPDAADSVWFRPYLLENANQLDTALQI
290      300      310      320      330      340      350      360

```

```

PAEIGITDVPAFRTEEPINGQDAIRIWESFTSGFRFTYVDSPOKOKKITYRIANMLASTVSLTNNQ
PAEIGITDVPAFRTEEPINGQDAIRIWESFTSGFRFTYVDSPOKOKKITYRIANMLASTVSLTNNQ
PAEIGITDVPAFRTEEPINGQDAIRIWESFTSGFRFTYVDSPOKOKKITYRIANMLASTVSLTNNQ
370      380      390      400      410      420      430

```

```

TFPTDILNTSLDPNGVRNGYGYTLVEGPIIEFSOGTNIPIKLSOGKGFADISITSPVY
TFPTDILNTSLDPNGVRNGYGYTLVEGPIIEFSOGTNIPIKLSOGKGFADISITSPVY
TFPTDILNTSLDPNGVRNGYGYTLVEGPIIEFSOGTNIPIKLSOGKGFADISITSPVY
440      450      460      470      480      490 X

```

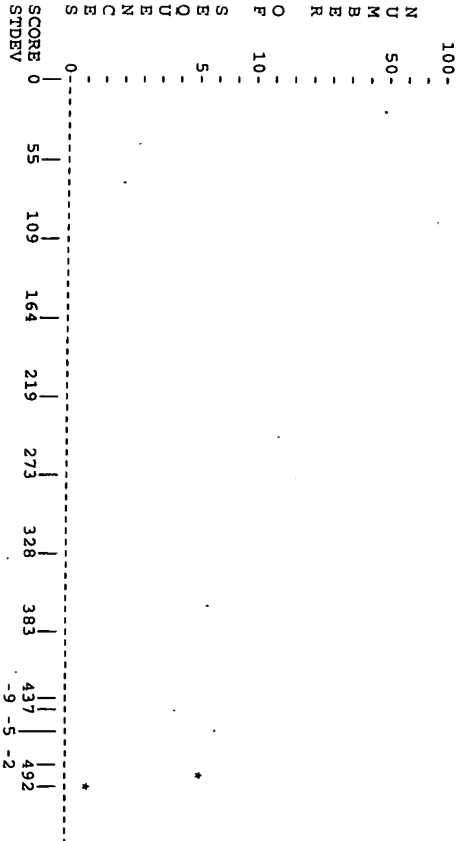

> O <
O | O < Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-756-778-8.res made by bshears on Thu 6 Apr 106 10:09:35-PST.

Query sequence being compared: US-10-756-778-8 (1-492)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-10-756-778-8 (1-492) with:
File: /home/bshears/rook*pep



Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 2
Gap penalty 1.00 Window size 20
Gap size penalty 0.05 32
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 479 478 6.12
Times: CPU Total Elapsed
 00:00:00.00 00:00:00.00

Number of residues: 3933
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% similar sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
---------------	-------------	--------	-------	-------	------	-------

The list of other best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame
---------------	-------------	--------	-------	------	-------

1.	US-10-756-778-2 Sequence 2, Application US	742	492	492	2.12	0
----	--	-----	-----	-----	------	---

2.	US-10-756-778-15 Sequence 15, Application	492	477	477	-0.33	0
3.	US-10-756-778-13 Sequence 13, Application	492	477	477	-0.33	0
4.	US-10-756-778-18 Sequence 18, Application	723	477	477	-0.33	0
5.	US-10-756-778-14 Sequence 14, Application	742	477	477	-0.33	0
6.	US-10-756-778-12 Sequence 12, Application	742	477	477	-0.33	0

1. US-10-756-778-8 (1-492)
US-10-756-778-2 Sequence 2, Application US/10756778

Sequence 2, Application US/10756778
GENERAL INFORMATION:

APPLICANT: Agriculture Agrolimentaire Canada
APPLICANT: Cote, Jean-Charles
APPLICANT: Mizuki, Eiichi
APPLICANT: Akao, Tetsuyuki
APPLICANT: Jung, Yong-Chul
TITLE OF INVENTION: A NOVEL BACILLUS THURINGIENSIS STRAIN, CRYSTAL GENE AND CRYSTAL
FILE REFERENCE: 12292.5
CURRENT APPLICATION NUMBER: US/10/756, 778
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 2,410,153
PRIOR FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent version 3.2
SEQ ID NO 2
LENGTH: 742
TYPE: PRT
ORGANISM: Bacillus thuringiensis

Initial Score = 492 Optimized Score = 492 Significance = 2.12
Residue identity = 100% Matches = 492 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

170	180	190	200	210	220	230	240
250	260	270	280	290	300	310	320
350	360	370	380	390	400	410	420
430	440	450	460	470	480	490	500
510	520	530	540	550	560	570	580
590	600	610	620	630	640	650	660
670	680	690	700	710	720	730	740
750	760	770	780	790	800	810	820
830	840	850	860	870	880	890	900
910	920	930	940	950	960	970	980
990	1000	1010	1020	1030	1040	1050	1060
1070	1080	1090	1100	1110	1120	1130	1140
1150	1160	1170	1180	1190	1200	1210	1220
1230	1240	1250	1260	1270	1280	1290	1300
1310	1320	1330	1340	1350	1360	1370	1380
1390	1400	1410	1420	1430	1440	1450	1460
1470	1480	1490	1500	1510	1520	1530	1540
1550	1560	1570	1580	1590	1600	1610	1620
1630	1640	1650	1660	1670	1680	1690	1700
1710	1720	1730	1740	1750	1760	1770	1780
1790	1800	1810	1820	1830	1840	1850	1860
1870	1880	1890	1900	1910	1920	1930	1940
1950	1960	1970	1980	1990	2000	2010	2020
2030	2040	2050	2060	2070	2080	2090	2100
2110	2120	2130	2140	2150	2160	2170	2180
2190	2200	2210	2220	2230	2240	2250	2260
2270	2280	2290	2300	2310	2320	2330	2340
2350	2360	2370	2380	2390	2400	2410	2420
2430	2440	2450	2460	2470	2480	2490	2500
2510	2520	2530	2540	2550	2560	2570	2580
2590	2600	2610	2620	2630	2640	2650	2660
2670	2680	2690	2700	2710	2720	2730	2740
2750	2760	2770	2780	2790	2800	2810	2820
2830	2840	2850	2860	2870	2880	2890	2900
2910	2920	2930	2940	2950	2960	2970	2980
2990	3000	3010	3020	3030	3040	3050	3060
3070	3080	3090	3100	3110	3120	3130	3140
3150	3160	3170	3180	3190	3200	3210	3220
3230	3240	3250	3260	3270	3280	3290	3300
3310	3320	3330	3340	3350	3360	3370	3380
3390	3400	3410	3420	3430	3440	3450	3460
3470	3480	3490	3500	3510	3520	3530	3540
3550	3560	3570	3580	3590	3600	3610	3620
3630	3640	3650	3660	3670	3680	3690	3700
3710	3720	3730	3740	3750	3760	3770	3780
3790	3800	3810	3820	3830	3840	3850	3860
3870	3880	3890	3900	3910	3920	3930	3940
3950	3960	3970	3980	3990	4000	4010	4020
4030	4040	4050	4060	4070	4080	4090	4100
4110	4120	4130	4140	4150	4160	4170	4180
4190	4200	4210	4220	4230	4240	4250	4260
4270	4280	4290	4300	4310	4320	4330	4340
4350	4360	4370	4380	4390	4400	4410	4420
4430	4440	4450	4460	4470	4480	4490	4500
4510	4520	4530	4540	4550	4560	4570	4580
4590	4600	4610	4620	4630	4640	4650	4660
4670	4680	4690	4700	4710	4720	4730	4740
4750	4760	4770	4780	4790	4800	4810	4820
4830	4840	4850	4860	4870	4880	4890	4900
4910	4920	4930	4940	4950	4960	4970	4980
4990	5000	5010	5020	5030	5040	5050	5060
5070	5080	5090	5100	5110	5120	5130	5140
5150	5160	5170	5180	5190	5200	5210	5220
5230	5240	5250	5260	5270	5280	5290	5300
5310	5320	5330	5340	5350	5360	5370	5380
5390	5400	5410	5420	5430	5440	5450	5460
5470	5480	5490	5500	5510	5520	5530	5540
5550	5560	5570	5580	5590	5600	5610	5620
5630	5640	5650	5660	5670	5680	5690	5700
5710	5720	5730	5740	5750	5760	5770	5780
5790	5800	5810	5820	5830	5840	5850	5860
5870	5880	5890	5900	5910	5920	5930	5940
5950	5960	5970	5980	5990	6000	6010	6020
6030	6040	6050	6060	6070	6080	6090	6100
6110	6120	6130	6140	6150	6160	6170	6180
6190	6200	6210	6220	6230	6240	6250	6260
6270	6280	6290	6300	6310	6320	6330	6340
6350	6360	6370	6380	6390	6400	6410	6420
6430	6440	6450	6460	6470	6480	6490	6500
6510	6520	6530	6540	6550	6560	6570	6580
6590	6600	6610	6620	6630	6640	6650	6660
6670	6680	6690	6700	6710	6720	6730	6740
6750	6760	6770	6780	6790	6800	6810	6820
6830	6840	6850	6860	6870	6880	6890	6900
6910	6920	6930	6940	6950	6960	6970	6980
6990	7000	7010	7020	7030	7040	7050	7060
7070	7080	7090	7100	7110	7120	7130	7140
7150	7160	7170	7180	7190	7200	7210	7220
7230	7240	7250	7260	7270	7280	7290	7300
7310	7320	7330	7340	7350	7360	7370	7380
7390	7400	7410	7420	7430	7440	7450	7460
7470	7480	7490	7500	7510	7520	7530	7540
7550	7560	7570	7580	7590	7600	7610	7620
7630	7640	7650	7660	7670	7680	7690	7700
7710	7720	7730	7740	7750	7760	7770	7780
7790	7800	7810	7820	7830	7840	7850	7860
7870	7880	7890	7900	7910	7920	7930	7940
7950	7960	7970	7980	7990	8000	8010	8020
8030	8040	8050	8060	8070	8080	8090	8100
8110	8120	8130	8140	8150	8160	8170	8180
8190	8200	8210	8220	8230	8240	8250	8260
8270	8280	8290	8300	8310	8320	8330	8340
8350	8360	8370	8380	8390	8400	8410	8420
8430	8440	8450	8460	8470	8480	8490	8500
8510	8520	8530	8540	8550	8560	8570	8580
8590	8600	8610	8620	8630	8640	8650	8660
8670	8680	8690	8700	8710	8720	8730	8740
8750	8760	8770	8780	8790	8800	8810	8820
8830	8840	8850	8860	8870	8880	8890	8900
8910	8920	8930	8940	8950	8960	8970	8980
8990	9000	9010	9020	9030	9040	9050	9060
9070	9080	9090	9100	9110	9120	9130	9140
9150	9160	9170	9180	9190	9200	9210	9220
9230	9240	9250	9260	9270	9280	9290	9300
9310	9320	9330	9340	9350	9360	9370	9380
9390	9400	9410	9420	9430	9440	9450	9460
9470	9480	9490	9500	9510	9520	9530	9540
9550	9560	9570	9580	9590	9600	9610	9620
9630	9640	9650	9660	9670	9680	9690	9700
9710	9720	9730	9740	9750	9760	9770	9780
9790	9800	9810	9820	9830	9840	9850	9860
9870	9880	9890	9900	9910	9920	9930	9940
9950	9960	9970	9980	9990	10000	10010	10020
10030	10040	10050	10060	10070	10080	10090	10100
10110	10120	10130	10140	10150	10160	10170	10180
10190	10200	10210	10220	10230	10240	10250	10260
10270	10280	10290	10300	10310	10320	10330	10340
10350	10360	10370	10380	10390	10400	10410	10420
10430	10440	10450	10460	10470	10480	10490	10500
10510	10520	10530	10540	10550	10560	10570	10580
10590	10600	10610	10620	10630	10640	10650	10660
10670	10680	10690	10700	10710	10720	10730	10740
10750	10760	10770	10780	10790	10800	10810	10820

PRIOR APPLICATION NUMBER: 2,410,153
 PRIOR FILING DATE: 2002-12-05
 NUMBER OF SEQ.ID NOS: 18
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 18
 LENGTH: 723
 TYPE: PRF
 ORGANISM: Bacillus thuringiensis

Initial Score = 477 Optimized Score = 477 Significance = -0.33
 Residue Identity = 96% Matches = 477 Mismatches = 15
 Gaps = 0 Conservative Substitutions = 0

ROMVDYERKIDSKLDYHNFIMGAELALNALKEVAVVVFENDNRRAAEPTSTGVITQFRLINDNFIX
 190 200 210 220 230 X 240 250
 30 40 50 60 70 80 90
 YIAQLQFSTNSDLOYPPLTLPRAQACVMEHMLKIDATTSVWGQIDSDQNGYKALRLIKVYNDVNT
 260 270 280 290 300 310 320
 YIALQFSTNSDLOYPPLTLPRAQACVMEHMLKIDATTSVWGQIDSDQNGYKALRLIKVYNDVNT
 100 110 120 130 140 150 160
 TYNGLELEKAKPLNYSPEBYLQAGRDIVLSNFEVEMKMNVAKYKKGMMASLSIALPPTGPNYP
 330 340 350 360 370 380 390
 TYNGLELEKAKPLNYSPEBYLQAGRDIVLSNFEVEMKMNVAKYKKGMMASLSIALPPTGPNYP
 170 180 190 200 210 220 230
 KOALKVQSRQIFAPVIGIPGITSQDSGPTFGSRFPVKTYYDIDALRLQELIYIOLKSAFYIYESDWK
 400 410 420 430 440 450 460
 KOALKVQSRQIFAPVIGIPGITSQDSGPTFGSRFPVKTYYDIDALRLQELIYIOLKSAFYIYESDWK
 240 250 260 270 280 290 300 310
 VRATYVNDYIGKRGSTGAAMHMSDDPSATYTSALGAGYAPNVGVYSHGGSYTKGMAPANTNAVPE
 470 480 490 500 510 520 530 540
 VRATYVNDYIGKRGSTGAAMHMSDDPSATYTSALGAGYAPNVGVYSHGGSYTKGMAPANTNAVPE
 320 330 340 350 360 370 380
 FKYPGYKLSHSAVGLSAPPAOSVMEGFVPLENANQLTDTALQIPAEIGITDVVAFKRTPEPING
 550 560 570 580 590 600 610
 FKYPGYKLSHSAVGLSAPPAOSVMEGFVPLENANQLTDTALQIPAEIGITDVVAFKRTPEPING
 390 400 410 420 430 440 450
 ODAIRIMESFTSGFGFTYTVDSPOKOKKIIYRIANNLSASTVSLTYNNQTFPDILNTSLDPNGVGNYS
 620 630 640 650 660 670 680
 ODAIRIMESFTSGFGFTYTVDSPOKOKKIIYRIANNLSASTVSLTYNNQTFPDILNTSLDPNGVGNYS
 460 470 480 490 X
 YTVVGPPIESGGINIFKLSQKGEFAIDSIIFSPV
 690 700 710 720 X
 YTVVGPPIESGGINIFKLSQKGEFAIDSIIFSPV

5. US-10-756-778-8 (1.492)
 US-10-756-778-14 Sequence 14, Application US/10756778

Sequence 14, Application US/10756778
 GENERAL INFORMATION:
 APPLICANT: Agriculture Agroalimentaire Canada
 APPLICANT: Cote, Jean-Charles
 APPLICANT: Mizuki, Eiichi
 APPLICANT: Akao, Tetsuyuki
 APPLICANT: Jung, Yong-Chul
 TITLE OF INVENTION: A NOVEL BACILLUS THURINGIENSIS STRAIN, CRYSTAL GENE AND CRYSTAL

TITLE OF INVENTION: PROTEIN AND USES THEREOF
 FILE REFERENCE: 12292.5
 CURRENT APPLICATION NUMBER: US/10/756, 778
 CURRENT FILING DATE: 2004-01-14
 PRIOR APPLICATION NUMBER: 2,410,153
 PRIOR FILING DATE: 2002-12-05
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 14
 LENGTH: 742
 TYPE: PRF
 ORGANISM: Bacillus thuringiensis

FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (24)..(24)
 OTHER INFORMATION: Xaa=glutamate or lysine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (37)..(37)
 OTHER INFORMATION: Xaa= methionine or alanine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (39)..(39)
 OTHER INFORMATION: Xaa= threonine or asparagine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (51)..(51)
 OTHER INFORMATION: Xaa= alanine or threonine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (56)..(56)
 OTHER INFORMATION: Xaa= proline or serine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (59)..(59)
 OTHER INFORMATION: Xaa= tyrosine or tryptophan
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (87)..(87)
 OTHER INFORMATION: Xaa= asparagine or aspartate
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (97)..(97)
 OTHER INFORMATION: Xaa= arginine or lysine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (138)..(138)
 OTHER INFORMATION: Xaa= glutamate or lysine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (158)..(158)
 OTHER INFORMATION: Xaa= alanine or asparagine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (170)..(170)
 OTHER INFORMATION: Xaa= glycine or serine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (251)..(251)
 OTHER INFORMATION: Xaa= isoleucine or methionine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (389)..(389)
 OTHER INFORMATION: Xaa= lysine or arginine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (444)..(444)
 OTHER INFORMATION: Xaa= serine or histidine
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (445)..(445)
 OTHER INFORMATION: Xaa= glycine or serine
 FEATURE:

NAME/KEY: MISC FEATURE
LOCATION: (446)..(446)
OTHER INFORMATION: Xaa= glycine or proline
FEATURE: MISC FEATURE
LOCATION: (466)..(466)
OTHER INFORMATION: Xaa= glutamine or arginine
FEATURE: MISC FEATURE
LOCATION: (481)..(481)
OTHER INFORMATION: Xaa= tyrosine or tryptophan
FEATURE: MISC FEATURE
LOCATION: (507)..(507)
OTHER INFORMATION: Xaa= alanine or leucine
FEATURE: MISC FEATURE
LOCATION: (510)..(510)
OTHER INFORMATION: Xaa= glycine or histidine
FEATURE: MISC FEATURE
LOCATION: (518)..(518)
OTHER INFORMATION: Xaa= alanine or valine
FEATURE: MISC FEATURE
LOCATION: (551)..(551)
OTHER INFORMATION: Xaa= alanine or proline
FEATURE: MISC FEATURE
LOCATION: (582)..(582)
OTHER INFORMATION: Xaa= alanine or threonine
FEATURE: MISC FEATURE
LOCATION: (637)..(637)
OTHER INFORMATION: Xaa= arginine or isoleucine
FEATURE: MISC FEATURE
LOCATION: (725)..(725)
OTHER INFORMATION: Xaa= glycine or arginine
FEATURE: MISC FEATURE
LOCATION: (742)..(742)
OTHER INFORMATION: Xaa= valine or serine

Initial Score = 477 Optimized Score = 477 Significance = -0.33
Residue Identity = 96% Matches = 477 Mismatches = 15
Gaps = 0 Conservative Substitutions = 0

RQWVDYVKEKIDSKILDYHNFIMGAEALANASLKEYARVVKIPENIMNKAABPSTGVITOFRIINDNFIK
210 220 230 240 250 260 270
X
IAEPPSTGVITOFRIINDNFIK
210 220 230 240 250 260 270

YIAKLGSTNOSDIQYVLTLPFAQACVHMLKADTTTSVWGQIDISQOLNGYKELIRLIKVTYNDVT
30 40 50 60 70 80 90
YIAKLGSTNOSDIQYVLTLPFAQACVHMLKADTTTSVWGQIDISQOLNGYKELIRLIKVTYNDVT
280 290 300 310 320 330 340

TYNGLLEKAKPLNYSDDPEEYLDAGRPDISVLSNFEKVMKVKAKYKGMWMSLSLALEPTGPNYP
100 110 120 130 140 150 160
TYNGLLEKAKPLNYSDDPEEYLDAGRPDISVLSNFEKVMKVKAKYKGMWMSLSLALEPTGPNYP
350 360 370 380 390 400 410

KOLKVTQSRQIFPAVIGIGITTSODSGPTFGSMRPDVKTQIDIALROLMEYIOLKSAFYFWIESDMK
170 180 190 200 210 220 230
KOLKVTQSRQIFPAVIGIGITTSODSGPTFGSMRPDVKTQIDIALROLMEYIOLKSAFYFWIESDMK
420 430 440 450 460 470 480

VBATVNDYIGKRGSNLTGAAMHMSDDPSAIYTSALGAAGYAPNVVGVRYHSGSYTKGMAPNTNAYAPFE
490 500 510 520 530 540 550 560
VBATVNDYIGKRGSNLTGAAMHMSDDPSAIYTSALGAAGYAPNVVGVRYHSGSYTKGMAPNTNAYAPFE
570 580 590 600 610 620 630
FKYPGKHSVSAVGLSKAPDAADSVMGFRPVLLNEANOLTTTALQIPAEIGITTVVPAFGTEEPING
320 330 340 350 360 370 380
FKYPGKHSVSAVGLSKAPDAADSVMGFRPVLLNEANOLTTTALQIPAEIGITTVVPAFGTEEPING
640 650 660 670 680 690 700
ODAIRWESFTSGFGTTVDSPOKOKIIRIANNLSASTVSLTNNQFFTLITSLDPNVRNGYS
390 400 410 420 430 440 450
ODAIRWESFTSGFGTTVDSPOKOKIIRIANNLSASTVSLTNNQFFTLITSLDPNVRNGYS
640 650 660 670 680 690 700
YTLVSGPIIEFSOGTNIPLKSGKGEPAIDSIIEFPV
460 470 480 490 X
YTLVSGPIIEFSOGTNIPLKSGKGEPAIDSIIEFPV
710 720 730 740 X

6. US-10-756-778-8 (1-492)
US-10-756-778-12 Sequence 12, Application US/10756778

Sequence 12, Application US/10756778
GENERAL INFORMATION:
APPLICANT: Agriculture Agrolimentaire Canada
APPLICANT: Cote, Jean-Charles
APPLICANT: Mizuki, Eichi
APPLICANT: Akao, Tetsuyuki
TITLE OF INVENTION: A NOVEL BACILLUS THURINGIENSIS STRAIN, CRYSTAL GENE AND CRYSTAL
FILE REFERENCE: 12292.5
CURRENT APPLICATION NUMBER: US/10/756,778
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 2,410,153
PRIOR FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 742
TYPE: PR1
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (24)..(24)
OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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NAME/KEY: MISC FEATURE
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OTHER INFORMATION: Xaa=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE

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OTHER INFORMATION: Xaa=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (725)..(725)

OTHER INFORMATION: Xaa=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (742)..(742)
OTHER INFORMATION: Xaa=any amino acid

Initial Score = 477 Optimized Score = 477 Significance = -0.33
Residue Identity = 96% Matches = 477 Mismatches = 15
Gaps = 0 Conservative Substitutions = 0

QDAIRIWESFTSGFGFTTYVDSPOKOKYIIIRIANLISASTVLSLTYNNQTFETDILNTSLDPNGVGYGS
QDAIXIWESFTSGFGFTTYVDSPOKOKYIIIRIANLISASTVLSLTYNNQTFETDILNTSLDPNGVGYGS
460 470 480 490 X
YTLVSGPIIEFSQGTNIIFKLGSOKGEFAIDSIIFSPV
YTLVSGPIIEFSQGTNIIFKLGSOKGEFAIDSIIFSPV
710 720 730 740 X

VRATVNDYIGKRGSTNGAAMHMSDPSAITYTSALGAGYAPNVVGYRYSHGSGYTKGMAAPNTNAYAPFE
VRATVNDYIGKRGSTNGAAMHMSDPSAITYTSALGAGYAPNVVGYRYSHGSGYTKGMAAPNTNAYAPFE
490 500 510 520 530 540 550 560

FKYRGYKLSHVSAYGLSKAPDADSVMEFGFRPVLLLENANQLTTALDIPAIIGITTDVVPAGRTTEEPING
FKYRGYKLSHVSAYGLSKAPDADSVMEFGFRPVLLLENANQLTTALDIPAIIGITTDVVPAGRTTEEPING
570 580 590 600 610 620 630

YIAKLOPSTNOSDLOYPVLTLPRAQACVHMLMLKDATTTSWGQOIDSQOLNGYAEILRLIKVTTNDVNT
YIAKLOPSTNOSDLOYPVLTLPRAQACVHMLMLKDATTTSWGQOIDSQOLNGYAEILRLIKVTTNDVNT
280 290 300 310 320 330 340

TYNOGLELEKAKPLINYSDBPEYLOAGRDPISVLRSNFKEVMKNKVAKYKRGAMASALIALFPFGPNYP
TYNOGLELEKAKPLINYSDBPEYLOAGRDPISVLRSNFKEVMKNKVAKYKRGAMASALIALFPFGPNYP
350 360 370 380 390 400 410

KOALKVQSRQIFAPVIGLPGGITTSODSGPTGSMRFVYKTYDDIDALQMLBELYIOPKSAIFMAYESDVK
KOALKVQSRQIFAPVIGLPGGITTSODSGPTGSMRFVYKTYDDIDALQMLBELYIOPKSAIFMAYESDVK
420 430 440 450 460 470 480

VRATVNDYIGKRGSTNGAAMHMSDPSAITYTSALGAGYAPNVVGYRYSHGSGYTKGMAAPNTNAYAPFE
VRATVNDYIGKRGSTNGAAMHMSDPSAITYTSALGAGYAPNVVGYRYSHGSGYTKGMAAPNTNAYAPFE
240 250 260 270 280 290 300 310

> O <
O| |O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-756-778-8.res made by behears on Thu 6 Apr 106 10:55:54-PST.

Query sequence being compared: US-10-756-778-8 (1-492)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-756-778-8 (1-492) with:
File: /home/behears/rook756778b.pep

```

100-
N -
U 50-
M -
B -
E -
R -
O 10-
S -
S -
E 5-
O -
U -
E -
N -
C -
E -
S -
SCORE 0 53 106 159 212 265 318 371 424 477
SIDEV

```

PARAMETERS

```

Similarity matrix      Unitary      K-tuple      2
Mismatch penalty      1          Joining penalty 20
Gap penalty           1.00       Window size      32
Gap size penalty      0.05
Cutoff score          0
Randomization group   0

```

SEARCH STATISTICS

```

Scores:      Mean      Median      Standard Deviation
            477          0          0.00

Times:      CPU      Total Elapsed
            00:00:00.00      00:00:00.00

Number of residues:      492
Number of sequences searched: 1
Number of scores above cutoff: 1

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The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame	Sig.
1. US-10-756-778-18	Sequence 18, Application	492	477	477	0.00

1. US-10-756-778-8 (1-492)
US-10-756-778-18 Sequence 18, Application US/10756778 → residues 232-723

Sequence 18, Application US/10756778
GENERAL INFORMATION:

APPLICANT: Agriculture Agroalimentaire Canada
APPLICANT: Cote, Jean-Charles
APPLICANT: Mizuki, Eichi
APPLICANT: Akao, Tetsuyuki
TITLE OF INVENTION: A NOVEL BACILLUS THURINGIENSIS STRAIN, CRYSTAL GENE AND CRYSTAL
FILE REFERENCE: 12292.5
CURRENT APPLICATION NUMBER: US/10/756,778
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 2,410,153
PRIOR FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent version 3.2
SEQ ID NO: 18
LENGTH: 723
TYPE: PRT
ORGANISM: Bacillus thuringiensis

Initial Score = 477 Optimized Score = 477 Significance = 0.00
Residue Identity = 96% Matches = 477 Mismatches = 15
Gaps = 0 Conservative Substitutions = 0

```

X 10 20 30 40 50 60 70
IAEPSTGVITOFRIINDFIKYIAKLOFSTNOSDLOYVLTLPRAQACVHMLLDATTSTVWGQIDSO
MAEPSTGVITOFRIINDFIKYIAKLOFSTNOSDLOYVLTLPRAQACVHMLLDATTSTVWGQIDSO
X 10 20 30 40 50 60 70

```

```

80 90 100 110 120 130 140
OLNGYKALIRLIKVTYNDVNTYNOGLEKAKPLNYSDEPEYLOAGRPIISVLRSPKESVMMKRVAKYK
OLNGYKALIRLIKVTYNDVNTYNOGLEKAKPLNYSDEPEYLOAGRPIISVLRSPKESVMMKRVAKYK
80 90 100 110 120 130 140

```

```

150 160 170 180 190 200 210
RGMASALSLALPFTFGPNYPKQALKVQSRQIFAPVIGIPGGITSDSGPTGSMRFDVKTQIDALRR
RGMASALSLALPFTFGPNYPKQALKVQSRQIFAPVIGIPGGITSDSGPTGSMRFDVKTQIDALRR
150 160 170 180 190 200 210

```

```

220 230 240 250 260 270 280
IMELYIOPKSAFYFWISDMKVRATYVNDYIGKSGNTGAAMHWSDEPAITYSALGAGYAPNVGVRY
IMELYIOPKSAFYFWISDMKVRATYVNDYIGKSGNTGAAMHWSDEPAITYSALGAGYAPNVGVRY
220 230 240 250 260 270 280

```

```

290 300 310 320 330 340 350
SHGSGYTKGMAMPNTNAAVAPEPFKPGKLSVSAVYGLSKAPDAADSVMPFRPVLLENENQLLTDLAI
SHGSGYTKGMAMPNTNAAVAPEPFKPGKLSVSAVYGLSKAPDAADSVMPFRPVLLENENQLLTDLAI
290 300 310 320 330 340 350

```

```

370 380 390 400 410 420 430
PAEIGITVPAFGRTSPINGQDAIIRIWESTSGFTYVDSPOKQYKIVIRIANLSASTVSLTVNO
PAEIGITVPAFGRTSPINGQDAIIRIWESTSGFTYVDSPOKQYKIVIRIANLSASTVSLTVNO
370 380 390 400 410 420 430

```

```

440 450 460 470 480 490 X
TFETDILNTSLDPNGVRNGYGYTLVBSPIIFSGCTNIIFKLGSGKGFALDISITFSRVV
TFETDILNTSLDPNGVRNGYGYTLVBSPIIFSGCTNIIFKLGSGKGFALDISITFSRVV

```

Thu Apr 6 10:58:44 2006

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Page 2

TFETDILNTSLDENGVRGNVGSYTLVIESPIIESQSOTNIFKLRSOKGEPAIDSIIFSPVS
440 450 460 470 480 490 X